```
              GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:  August 17, 2005, 20:11:47 ; Search time 176 Seconds
                                     (without alignments)
                                     2129.784 Million cell updates/sec

Title:      US-10-768-030-1
Perfect score:  3761
Sequence:   1 MVRSGNKAAVVLCMDVGFTM.........GDTAAVPEGGDVDDILDMI 732

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:  1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  UniProt 03:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3756	99.9	731	1	KU86_HUMAN	P13010 h atp-depen
2	2971	79.0	732	2	Q60449	Q60449 cricetulus
3	2971	79.0	732	2	Q60530	Q60530 mesocricetu
4	2939	78.1	732	2	Q80UT1	Q80UT1 mus musculu
5	2937	78.1	731	2	Q8K1K7	Q8K1K7 mus musculu
6	2932	78.0	732	2	Q9R169	Q9R169 mus musculu
7	2922	77.7	732	2	Q6P7P8	Q6P7P8 rattus norv
8	2893	76.9	732	1	KU86_MOUSE	P27641 mus musculu
9	2865.5	76.2	708	2	Q8C4N6	Q8C4N6 mus musculu
10	2748	73.1	683	2	Q8VIB0	Q8VIB0 rattus norv
11	2339	62.2	726	2	Q6DDS9	Q6DDS9 xenopus lae
12	2327	61.9	726	2	Q9W627	Q9W627 xenopus lae
13	1065	28.3	283	2	Q9CRI5	Q9CRI5 mus musculu
14	694	18.5	138	2	Q6UIL6	Q6UIL6 pan troglod
15	688	18.3	138	2	Q6UIL5	Q6UIL5 macaca mula
16	585	15.6	683	2	Q8S563	Q8S563 medicago tr
17	569	15.1	686	2	Q8S562	Q8S562 phaseolus v
18	540.5	14.4	593	2	Q7Q190	Q7Q190 anopheles g
19	525	14.0	680	2	Q9FQ09	Q9FQ09 arabidopsis
20	525	14.0	688	2	Q75IP6	Q75IP6 oryza sativ
21	496	13.2	663	2	Q9C7Z3	Q9C7Z3 arabidopsis
22	459	12.2	707	2	Q9LNF5	Q9LNF5 arabidopsis
23	418.5	11.1	661	2	Q7RX73	Q7RX73 neurospora
24	402.5	10.7	145	2	Q90ZQ9	Q90ZQ9 oryzias lat
25	344	9.1	726	2	Q6C7B9	Q6C7B9 yarrowia li
26	342	9.1	695	2	Q9HGM8	Q9HGM8 schizosacch
27	318.5	8.5	699	2	Q8MSM8	Q8MSM8 drosophila
28	318.5	8.5	699	2	Q9NGX6	Q9NGX6 drosophila
29	316.5	8.4	699	2	Q917M8	Q917M8 drosophila
30	309.5	8.2	904	2	Q9NK79	Q9NK79 drosophila
31	294.5	7.8	728	2	Q21829	Q21829 caenorhabdi
32	233	6.2	325	2	Q75IP5	Q75IP5 oryza sativ
33	203	5.4	40	2	Q9UCQ1	Q9UCQ1 homo sapien
34	180	4.8	585	2	Q6CCK2	Q6CCK2 yarrowia li
35	173	4.6	608	2	Q8QZX7	Q8QZX7 mus musculu
36	172	4.6	615	2	Q6FN20	Q6FN20 candida gla
37	172	4.6	645	2	Q7SA95	Q7SA95 neurospora
38	171	4.5	723	2	Q6BXN4	Q6BXN4 debaryomyce
39	170	4.3	608	1	KU70_MOUSE	P23475 mus musculu
40	161.5	4.3	600	1	KU70_RHIAP	Q26228 rhipicephal
41	157.5	4.2	634	2	Q95PL8	Q95PL8 trypanosoma
42	157.5	4.2	1370	1	Q6A078	Q6A078 mus musculu
43	152	4.0	3065	2	Q70WN3	Q70WN3 peru tomato
44	151	4.0	608	2	Q9QVN9	Q9QVN9 cricetulus
45	150.5	4.0	629	1	KU80_YEAST	Q04437 saccharomyc

ALIGNMENTS

```
RESULT 1
KU86_HUMAN
ID   KU86_HUMAN     STANDARD;      PRT;   731 AA.
AC   P13010;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   ATP-dependent DNA helicase II, 80 kDa subunit (Lupus Ku autoantigen
DE   protein p86) (Ku80) (86 kDa subunit of Ku antigen) (Thyroid-
DE   lupus autoantigen) (TLAA) (CTC box binding factor 85 kDa subunit)
DE   (CTCBF) (CTC85) (Nuclear factor IV) (DNA-repair protein XRCC5).
GN   Name=XRCC5; Synonyms=G22P2;
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 3-21.
RX   MEDLINE=89340410; PubMed=2760028;
RA   Yaneva M., Wen J., Ayala A., Cook R.;
RT   "cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku
RT   antigen.";
RL   J. Biol. Chem. 264:13407-13411(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90175380; PubMed=2308937;
RA   Mimori T., Ohosone Y., Hama N., Suwa A., Akizuki M., Homma M.,
RA   Griffith A.J., Hardin J.A.;
RT   "Isolation and characterization of cDNA encoding the 80-kDa subunit
RT   of the human autoantigen Ku (p70/p80) recognized by
RT   autoantibodies from patients with scleroderma-polymyositis overlap
RT   syndrome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:1777-1781(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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OM protein - protein search, using sw model

Run on:     August 17, 2005, 20:12:52 ; Search time 44 Seconds
                                        (without alignments)
                                        1600.697 Million cell updates/sec

Title:          US-10-768-030-1
Perfect score:  3761
Sequence:       1 MVRSGNKAAVVLCMDVGFTM.........GDTAAVFBEGGDVDDLLDMI 732

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_79:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3761	100.0	732	2	A32626	Ku antigen 80K cha
2	2971	79.0	732	2	JC0099	Ku autoantigen 86k
3	2893	76.9	732	2	S26303	Ku autoantigen 80K
4	459	12.2	707	2	G96520	protein F21D18.26
5	294.5	7.8	728	2	S43606	R07E5.8 protein (c
6	175	4.7	595	2	A43534	Lupus autoantigen
7	161.5	4.3	600	2	S65788	Ku antigen 70K cha
8	150.5	4.0	629	2	S54567	hypothetical prote
9	146.5	3.9	1055	2	H64577	type I restriction
10	145	3.9	607	2	T40906	probable ATP-depen
11	143.5	3.8	1356	2	S32763	kinectin 1 - human
12	142	3.8	602	2	S54591	DNA-binding factor
13	141	3.7	1939	2	T18372	repeat organellar
14	138	3.7	1300	2	I53799	CG1 protein - huma
15	135.5	3.6	2094	2	S33124	tpr protein - huma
16	135	3.6	1496	2	T00499	probable retroelem
17	134	3.6	1927	2	G64585	cag pathogenicity
18	134	3.6	2166	2	G70163	hypothetical prote
19	132.5	3.5	871	2	B97035	DNA polymerase I,
20	132	3.5	1440	2	T33813	hypothetical prote
21	132	3.5	1642	2	T08880	NMDA receptor-bind
22	131	3.5	609	2	A30894	70K thyroid autoan
23	131	3.5	950	2	A71655	hypothetical prote
24	129	3.4	607	2	D86305	hypothetical prote
25	129	3.4	1087	2	T30330	gelsolin-related p
26	129	3.4	1538	2	T29095	cardiac muscle fac
27	127.5	3.4	990	2	H88733	protein F32E10.3 [
28	127	3.4	904	2	T03806	hypothetical prote
29	127	3.4	1837	2	T41023	probable nuclear p
30	127	3.4	2401	2	T28676	rhoptry protein -
31	126.5	3.4	910	2	S40259	glucose-6-phosphat
32	126.5	3.4	1295	2	T24587	hypothetical prote
33	126	3.4	1076	2	C70007	hypothetical prote
34	126	3.4	2469	2	H36812	hypothetical prote
35	125	3.3	1222	2	S56030	SCP160 protein - y
36	125	3.3	1819	2	A71928	cag island protein
37	124.5	3.3	759	2	D71853	hypothetical prote
38	124.5	3.3	939	2	B90558	topoisomerase iv s
39	124.5	3.3	1790	2	S67593	transport protein
40	124.5	3.3	2104	2	T38774	myosin-3 heavy cha
41	124	3.3	819	2	E70105	P115 protein homol
42	124	3.3	2471	2	T42977	large tegument pro
43	123.5	3.3	550	2	T43196	probable glucose-6
44	123.5	3.3	1178	2	S54073	probable membrane
45	123	3.3	2139	2	T18296	myosin heavy chain

ALIGNMENTS

```
RESULT 1
A32626
Ku antigen 80K chain - human
N;Alternate names: CTC 85 protein; DNA-dependent ATPase 83k chain; Ku autoantigen; nucl
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A35051; JH0322; A39235; C42397; S54273; A54197
R;Mimori, T.; Ohosone, Y.; Hama, N.; Suwa, A.; Akizuki, M.; Homma, M.; Griffith, A.J.; l
  Proc. Natl. Acad. Sci. U.S.A. 87, 1777-1781, 1990
A;Title: Isolation and characterization of cDNA encoding the 80-kDa subunit protein of t
lap syndrome.
A;Reference number: A35051; MUID:90175380; PMID:2308937
A;Accession: A35051
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <MIM>
A;Cross-references: UNIPROT:P13010; GB:M30938; NID:g186793; PIDN:AAA36154.1; PID:g30709.
R;Yaneva, M.; Wen, J.; Ayala, A.; Cook, R.
J. Biol. Chem. 264, 13407-13411, 1989
A;Title: cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku antigen.
A;Reference number: A32626; MUID:89340410; PMID:2760028
A;Accession: A32626
A;Molecule type: mRNA
A;Residues: 1-732 <YAN>
A;Cross-references: GB:J04977; NID:g186791; PIDN:AAA59475.1; PID:g307093
R;Stulver, M.H.; Coenjaerts, F.E.J.; van der Vliet, P.C.
J. Exp. Med. 172, 1049-1054, 1990
A;Title: The autoantigen Ku is indistinguishable from NF IV, a protein forming multimer:
A;Reference number: JH0322; MUID:91011245; PMID:2212941
A;Accession: JH0322
A;Molecule type: mRNA
A;Residues: 105-732 <STU>
A;Experimental source: strain NTera 2D1
R;Knuth, M.W.; Gunderson, S.I.; Thompson, N.B.; Strasheim, L.A.; Burgess, R.R.
J. Biol. Chem. 265, 17911-17920, 1990
A;Title: Purification and characterization of proximal sequence element-binding protein
man U1 promoter.
A;Reference number: A39235; MUID:91009259; PMID:2211668
A;Accession: A39235
A;Molecule type: protein
A;Residues: 2-12,'X',14-22 <KNU>
R;Wedrychowski, A.; Henzel, W.; Huston, L.; Paslidis, N.; Ellerson, D.; McRae, M.; Seon
J. Biol. Chem. 267, 4533-4540, 1992
A;Title: Identification of proteins binding to interferon-inducible transcriptional enh
A;Reference number: A42397; MUID:92165807; PMID:1537839
A;Accession: C42397
A;Status: preliminary
A;Molecule type: protein
A;Residues: 526-565 <WED>
A;Experimental source: K562 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:85281)
R;Genersch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.
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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:15:42 ; Search time 166 Seconds
(without alignments)
1726.753 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAAVVLCMDVGPTM..........GDTAAVPEBGGDVDDLLDMI 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Published Applications AA:*
1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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3: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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21: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3761	100.0	732	14	US-10-097-340-363	Sequence 363, App
2	3761	100.0	732	15	US-10-116-275-169	Sequence 169, App
3	3761	100.0	732	16	US-10-408-765A-1124	Sequence 1124, Ap
4	3761	100.0	732	17	US-10-768-030-1	Sequence 1, Appli
5	3761	100.0	741	9	US-09-833-790-432	Sequence 432, App
6	3756	99.9	731	14	US-10-160-748-7	Sequence 7, Appli
7	2971	79.0	732	14	US-10-160-748-4	Sequence 4, Appli
8	2971	79.0	732	14	US-10-160-748-5	Sequence 5, Appli
9	2893	76.9	732	14	US-10-160-748-6	Sequence 6, Appli
10	2545.5	67.7	521	9	US-09-805-020-38	Sequence 38, Appl
11	2530	67.3	497	9	US-09-805-020-37	Sequence 37, Appl
12	545	14.5	721	15	US-10-425-114-62759	Sequence 62759, A Appli
13	543	14.4	681	14	US-10-160-748-2	Sequence 2, Appli
14	537	14.3	681	16	US-10-425-115-357314	Sequence 357314,
15	489	13.0	132	9	US-09-925-301-1530	Sequence 1530, Ap
16	390.5	10.4	631	16	US-10-437-963-133099	Sequence 133099,
17	339	9.0	64	9	US-09-864-761-35456	Sequence 35456, A
18	294.5	7.8	728	15	US-10-369-493-5694	Sequence 5694, Ap
19	293	7.8	56	9	US-09-864-761-37696	Sequence 37696, A
20	288	7.7	55	9	US-09-864-761-34694	Sequence 34694, A
21	288	7.7	55	9	US-09-864-761-36475	Sequence 36475, A
22	288	7.7	55	9	US-09-864-761-42907	Sequence 42907, A
23	283	7.5	292	16	US-10-425-115-357315	Sequence 357315,
24	239	6.4	379	15	US-10-424-599-188014	Sequence 188014,
25	221	5.9	44	9	US-09-864-761-35402	Sequence 35402, A
26	219	5.8	42	14	US-10-189-437-548	Sequence 548, App
27	184	4.9	673	15	US-10-369-493-13409	Sequence 13409, A
28	171	4.5	638	15	US-10-369-493-3523	Sequence 3523, Ap
29	169.5	4.5	190	15	US-10-425-114-52621	Sequence 52621, A
30	159	4.2	136	16	US-10-767-701-54545	Sequence 54545, A
31	151	3.9	166	15	US-10-424-599-278336	Sequence 278336,
32	147	3.9	142	15	US-10-424-599-167597	Sequence 167597,
33	146.5	3.9	1055	10	US-09-882-227-596	Sequence 596, App
34	142	3.8	602	15	US-10-369-493-1922	Sequence 1922, Ap
35	141	3.7	1939	17	US-10-732-923-3340	Sequence 3340, Ap
36	140	3.7	5317	16	US-10-668-767-59	Sequence 59, Appl
37	139	3.7	1881	14	US-10-032-585-7646	Sequence 7646, Ap
38	138	3.7	1300	16	US-10-408-765A-257	Sequence 257, App
39	136.5	3.6	113	16	US-10-767-701-54564	Sequence 54564, A
40	136.5	3.6	2654	14	US-10-227-610-2	Sequence 2, Appli
41	136	3.6	730	16	US-10-437-963-179929	Sequence 179929,
42	136	3.6	799	15	US-10-369-493-20654	Sequence 20654, A
43	135.5	3.6	684	16	US-10-425-115-357245	Sequence 357245,
44	135.5	3.6	841	16	US-10-425-115-231005	Sequence 231005,
45	134.5	3.6	715	16	US-10-408-765A-2096	Sequence 2096, Ap

ALIGNMENTS

RESULT 1
US-10-097-340-363
; Sequence 363, Application US/10097340
; Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel B. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26

OM protein - protein search, using sw model

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              GenCore version 5.1.6
       Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: August 17, 2005, 20:11:01 ; Search time 24 Seconds
(without alignments)
2276.796 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAAVVLCMDVGFTM........GDTAAVPEGGDVDDLLDMI 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	3761	100.0	732	4	US-09-569-037-7	Sequence 7, Appli
2	3761	100.0	732	4	US-09-949-016-7000	Sequence 7000, Ap
3	3761	100.0	743	4	US-09-949-016-11192	Sequence 11192, A
4	3756	99.9	731	4	US-10-160-748-7	Sequence 7, Appli
5	3730	99.2	820	3	US-09-173-914-2	Sequence 2, Appli
6	2971	79.0	732	4	US-10-160-748-4	Sequence 4, Appli
7	2971	79.0	732	4	US-10-160-748-5	Sequence 5, Appli
8	2893	76.9	732	4	US-10-160-748-6	Sequence 6, Appli
9	700	18.6	137	4	US-09-513-999C-5706	Sequence 5706, Ap
10	543	14.4	681	4	US-10-160-748-2	Sequence 2, Appli
11	394	10.5	78	4	US-09-569-037-16	Sequence 16, Appl
12	314.5	8.4	77	4	US-09-569-037-17	Sequence 17, Appl
13	314.5	8.4	77	4	US-09-569-037-18	Sequence 18, Appl
14	294.5	7.8	728	4	US-09-569-037-8	Sequence 8, Appli
15	174	4.6	34	4	US-09-569-037-11	Sequence 11, Appl
16	161.5	4.3	600	4	US-09-569-037-4	Sequence 4, Appli
17	150.5	4.0	629	4	US-09-569-037-9	Sequence 9, Appli
18	141	3.7	602	4	US-09-569-037-6	Sequence 6, Appli
19	139.5	3.7	531	4	US-09-248-796A-19139	Sequence 19139, A
20	138	3.7	1307	4	US-09-949-016-7561	Sequence 7561, Ap
21	137.5	3.7	650	3	US-09-385-801-2	Sequence 2, Appli
22	135.5	3.6	2186	4	US-09-949-016-10828	Sequence 10828, A
23	135.5	3.6	2349	4	US-09-538-092-914	Sequence 914, App
24	131	3.5	608	3	US-08-360-107A-126	Sequence 126, App
25	131	3.5	609	4	US-09-569-037-2	Sequence 2, Appli
26	130	3.5	1010	3	US-09-134-001C-5178	Sequence 5178, Ap
27	129.5	3.4	607	3	US-08-486-099-116	Sequence 116, App
28	129.5	3.4	607	3	US-08-484-223B-116	Sequence 116, App
29	129.5	3.4	607	3	US-08-919-597-116	Sequence 116, App
30	129.5	3.4	607	3	US-08-475-668A-116	Sequence 116, App
31	129.5	3.4	607	3	US-08-485-551A-116	Sequence 116, App
32	129.5	3.4	607	3	US-08-471-913A-116	Sequence 116, App
33	129.5	3.4	607	3	US-08-485-264A-116	Sequence 116, App
34	129.5	3.4	607	3	US-08-474-349A-116	Sequence 116, App
35	129.5	3.4	607	4	US-08-470-896-116	Sequence 116, App
36	129.5	3.4	607	4	US-08-485-546A-116	Sequence 116, App
37	129.5	3.4	607	4	US-08-487-266A-116	Sequence 116, App
38	127	3.4	904	3	US-09-198-484-2	Sequence 2, Appli
39	126	3.4	3878	4	US-09-914-259-11	Sequence 11, Appl
40	125	3.3	862	4	US-09-248-796A-16013	Sequence 16013, A
41	122	3.2	1234	4	US-09-592-054-8	Sequence 8, Appli
42	121	3.2	1346	4	US-09-949-016-9959	Sequence 9959, Ap
43	120	3.2	636	4	US-09-248-796A-14866	Sequence 14866, A
44	119.5	3.2	495	3	US-09-198-484-4	Sequence 4, Appli
45	119.5	3.2	2871	4	US-09-538-092-936	Sequence 936, App

ALIGNMENTS

RESULT 1
US-09-569-037-7
; Sequence 7, Application US/09569037
; Patent No. 6753151
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stephen P
; APPLICANT: Gell, David A
; TITLE OF INVENTION: Interactions of Ku polypeptides and applications
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 620-100
; CURRENT APPLICATION NUMBER: US/09/569,037
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: PCT/GB00/01245
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: GB 9907687.9
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-037-7

Query Match 100.0%; Score 3761; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MVRSGNKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAENKDEIALVLFG 60
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Db    1 MVRSGNKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAENKDEIALVLFG 60

Qy   61 TDGTDNPLSGGDQYQNITVHRHLMLPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQH 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TDGTDNPLSGGDQYQNITVHRHLMLPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQH 120

Qy  121 ETIGKKFEKRHIEIFTDLSSRFSKSQLDIIHSLKKCDISLQFFLPFSLGKEDGSGDRGD 180
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Db  121 ETIGKKFEKRHIEIFTDLSSRFSKSQLDIIHSLKKCDISLQFFLPFSLGKEDGSGDRGD 180

Qy  181 GPFRLGGHGPSFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLCVFKKI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GPFRLGGHGPSFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLCVFKKI 240

Qy  241 ERHSIHWPCRLTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
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Db  241 ERHSIHWPCRLTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300

Qy  301 DETEVLKEDIIQGFRYGSDIVPFSKVDBEQMKYKSEBGKCFSVLGFCKSSQVQRRFPMGNQ 360
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        GenCore version 5.1.6
    Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:08:01 ; Search time 165 Seconds
                                     (without alignments)
                        1715.810 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAAVVLCMDVGFTM.........GDTAAVFEGGDVDDLLDMI 732

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3761	100.0	732	5	ABG96452	Abg96452 Human ova
2	3761	100.0	732	7	ADJ69318	Adj69318 Human hea
3	3761	100.0	732	8	ADP43915	Adp43915 Human DNA
4	3761	100.0	732	8	ADQ14382	Adq14382 Human lup
5	3761	100.0	732	8	ABM80379	Abm80379 Tumour-as
6	3761	100.0	732	8	ADR97394	Adr97394 Human XRC
7	3761	100.0	732	8	ADS14356	Ads14356 Human lup
8	3761	100.0	741	5	AAU69427	Aau69427 Lung smal
9	3756	99.9	731	8	ADJ66474	Adj66474 ATP-depen
10	3754	99.8	732	8	ADR41763	Adr41763 Protein s
11	3730	99.2	820	4	AAB66590	Aab66590 Human KAR
12	3688	98.1	732	4	AAB29307	Aab29307 Human Ku8
13	3354	89.2	757	4	ABG08315	Abg08315 Novel hum
14	3221	85.6	628	6	ABU07475	Abu07475 Protein d
15	2893	76.9	732	2	AAW40496	Aaw40496 Mouse XRC
16	2545.5	67.7	521	5	ABG79671	Abg79671 Tumour in
17	2530	67.3	497	5	ABG79670	Abg79670 Tumour in
18	2454	65.2	644	2	AAW40497	Aaw40497 Mouse XRC
19	1784	47.4	384	4	ABG08312	Abg08312 Novel hum
20	1034.5	27.5	710	4	ABG08311	Abg08311 Novel hum
21	926.5	24.6	210	6	ABG99983	Abg99983 Human nov
22	700	18.6	137	3	AAG01625	Aag01625 Human sec
23	658.5	17.5	138	4	ABG08310	Abg08310 Novel hum
24	543	14.4	681	3	AAB19283	Aab19283 Amino aci
25	489	13.0	132	3	AAB44085	Aab44085 Human can
26	339	9.0	64	4	AAM15746	Aam15746 Peptide #
27	339	9.0	64	4	ABB34744	Abb34744 Peptide #
28	339	9.0	64	4	AAM28255	Aam28255 Peptide #
29	339	9.0	64	4	ABB29565	Abb29565 Peptide #
30	339	9.0	64	4	ABB20158	Abb20158 Protein #
31	339	9.0	64	4	AAM67928	Aam67928 Human bon
32	339	9.0	64	4	AAM55544	Aam55544 Human bra
33	339	9.0	64	4	ABG49572	Abg49572 Human liv
34	339	9.0	64	4	AAM03480	Aam03480 Peptide #
35	339	9.0	64	5	ABG37463	Abg37463 Human pep
36	316.5	8.4	699	8	ABB67287	Abb67287 Drosophil
37	294.5	7.8	728	8	ADN23041	Adn23041 Bacterial
38	293	7.8	56	4	AAM18049	Aam18049 Peptide #
39	293	7.8	56	4	ABB37087	Abb37087 Peptide #
40	293	7.8	56	4	AAM30563	Aam30563 Peptide #
41	293	7.8	56	4	ABB31853	Abb31853 Peptide #
42	293	7.8	56	4	ABB22398	Abb22398 Protein #
43	293	7.8	56	4	AAM70224	Aam70224 Human bon
44	293	7.8	56	4	AAM57810	Aam57810 Human bra
45	293	7.8	56	4	ABG51923	Abg51923 Human liv

ALIGNMENTS

RESULT 1
ABG96452
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ID   ABG96452 standard; protein; 732 AA.
XX
AC   ABG96452;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Human ovarian cancer marker M480.
XX
KW   Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW   central nervous system disorder; bacterial meningitis; viral meningitis;
KW   Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW   brain herniation; inflammation; encephalitis; testicular disorder;
KW   nontuberculous granulomatous orchitis; connective tissue disorder;
KW   heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW   histological type; carcinogenic; ovarian cancer marker.
XX
OS   Homo sapiens.
XX
PN   WO20271928-A2.
XX
PD   19-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-US007826.
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PR   14-MAR-2001; 2001US-0276025P.
PR   14-MAR-2001; 2001US-0276026P.
PR   10-AUG-2001; 2001US-0311732P.
PR   19-SEP-2001; 2001US-0323580P.
PR   26-SEP-2001; 2001US-0324967P.
PR   26-SEP-2001; 2001US-0325102P.
PR   26-SEP-2001; 2001US-0325149P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Monahan JB, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI   Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
PI   Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX
DR   WPI; 2002-723277/78.
DR   N-PSDB; ABS76552.
XX
PT   Assessing whether a patient is afflicted with ovarian cancer, useful in
PT   assessing the stage or progression of the disease, comprises comparing
PT   the expression level of a cancer marker in a sample from a patient and
PT   from a non cancer patient.
XX
```